

AMENDMENTS TO THE CLAIMS

1-33. Cancelled.

34. (New) A method of mass spectrometry, comprising:
exposing a sample containing a protein to a substrate;
allowing the protein to become immobilized with respect to the substrate;
exposing the protein immobilized with respect to the substrate to mass spectral ionization conditions to generate ionized fragments;
determining, via analysis of the identity of the ionized fragments, the identity of the protein.

35. (New) A method as in claim 34, wherein the sample contains a mixture of proteins, the method comprising, prior to exposing and determining:
exposing the sample containing a mixture of proteins to a substrate;
allowing the at least one protein to become immobilized with respect to the substrate;
and
removing any non-bound protein from the substrate.

36. (New) The method of claim 34, wherein the exposing step comprises exposing the protein immobilized to mass spectral ionization conditions using MALDI mass spectrometry.

37. (New) The method of claim 36, wherein the exposing step comprises exposing the protein immobilized to mass spectral ionization conditions using MALDI TOF mass spectrometry.

38. (New) The method of claim 34, wherein the determining step comprises determining the species using a first mass spectrometry technique and a second mass spectrometry technique.

39. (New) The method of claim 34, wherein the determining step comprises determining at least a portion of a primary sequence of the protein.

40. (New) The method of claim 34, wherein the protein is part of a mixture of substances.
41. (New) The method of claim 40, wherein the mixture comprises cell lysate.
42. (New) The method of claim 34, wherein the substrate includes a microarray.
43. (New) The method of claim 34, wherein the substrate includes a protein array.
44. (New) The method of claim 34, wherein the substrate includes a self-assembled monolayer.
45. (New) The method of claim 34, wherein the substrate includes a gold surface.
46. (New) The method of claim 34, wherein the protein is able to specifically bind to an entity that is bonded to the substrate.
47. (New) The method of claim 46, wherein the entity is an antibody.
48. (New) The method of claim 46, wherein each entity is individually addressable by mass spectrometry.
49. (New) A method of mass spectrometry, comprising:
exposing a mixture of proteins to a substrate;
allowing at least one protein to become immobilized with respect to the substrate;
removing any non-bound protein from the substrate;
exposing the at least one protein immobilized with respect to the substrate to an ionization method to generate ionized fragments; and

determining, via mass spectrometry of the identity of the ionized fragments, the identity of the at least one protein.